

Fig. 1. Alignment of amino acid sequences of human $G\alpha_q$, $G\alpha_{15}$ and $G\alpha_{16}$ by Clustal method.

The matched residues are marked in shaded box. The sequence accession number in the GenBank database is AAB06875, P30678, and P30679 for h $G\alpha_q$, $G\alpha_{15}$, and $G\alpha_{16}$ respectively.

1	M	T	L	E	S	I	M	A	C	C	-	-	-	L	S	E	E	A	K	E	A	R	R	I	N	D	E	I	E	R	Q	L	R	R	D	K	R	D	A	R		hGq
1	M	A	R	S	L	T	W	G	C	C	P	W	C	L	T	E	E	E	K	T	A	A	R	I	D	Q	E	I	N	R	I	L	L	E	Q	K	K	Q	E	R		G15
1	M	A	R	S	L	T	W	R	C	C	P	W	C	L	T	E	D	E	K	A	A	A	R	V	D	Q	E	I	N	R	I	L	L	E	Q	K	K	Q	D	R		G16
38	R	E	L	K	L	L	L	L	G	T	G	E	S	G	K	S	T	F	I	K	Q	M	R	I	I	H	G	S	G	Y	S	D	E	D	K	R	G	F	T	K		hGq
41	E	E	L	K	L	L	L	L	G	P	G	E	S	G	K	S	T	F	I	K	Q	M	R	I	I	H	G	V	G	Y	S	E	E	D	R	R	A	F	R	L		G15
41	G	E	L	K	L	L	L	L	G	P	G	E	S	G	K	S	T	F	I	K	Q	M	R	I	I	H	G	A	G	Y	S	E	E	E	R	K	G	F	R	P		G16
78	L	V	Y	Q	N	I	F	T	A	M	Q	A	M	I	R	A	M	D	T	L	K	I	P	Y	K	Y	E	H	N	K	A	H	A	Q	L	V	R	E	V	D		hGq
81	L	I	Y	Q	N	I	F	V	S	M	Q	A	M	I	D	A	M	D	R	L	Q	I	P	F	S	R	P	D	S	K	Q	H	A	S	L	V	M	T	Q	D		G15
81	L	V	Y	Q	N	I	F	V	S	M	R	A	M	I	E	A	M	E	R	L	Q	I	P	F	S	R	P	E	S	K	H	H	A	S	L	V	M	S	Q	D		G16
118	V	E	K	V	S	A	F	E	N	P	Y	V	D	A	I	K	S	L	W	N	D	P	G	I	Q	E	C	Y	D	R	R	R	E	Y	Q	L	S	D	S	T		hGq
121	P	Y	K	V	S	T	F	E	K	P	Y	A	V	A	M	Q	Y	L	W	R	D	A	G	I	R	A	C	Y	E	R	R	R	E	F	H	L	L	D	S	A		G15
121	P	Y	K	V	T	T	F	E	K	R	Y	A	A	A	M	Q	W	L	W	R	D	A	G	I	R	A	C	Y	E	R	R	R	E	F	H	L	L	D	S	A		G16
158	K	Y	Y	L	N	D	L	D	R	V	A	D	P	A	Y	L	P	T	Q	Q	D	V	L	R	V	R	V	P	T	T	G	I	I	E	Y	P	F	D	L	Q		hGq
161	V	Y	Y	L	S	H	L	E	R	I	S	E	D	S	Y	I	P	T	A	Q	D	V	L	R	S	R	M	P	T	T	G	I	N	E	Y	C	F	S	V	K		G15
161	V	Y	Y	L	S	H	L	E	R	I	T	E	E	G	Y	V	P	T	A	Q	D	V	L	R	S	R	M	P	T	T	G	I	N	E	Y	C	F	S	V	Q		G16
198	S	V	I	F	R	M	V	D	V	G	G	Q	R	S	E	R	R	K	W	I	H	C	F	E	N	V	T	S	I	M	F	L	V	A	L	S	E	Y	D	Q		hGq
201	K	T	K	L	R	I	V	D	V	G	G	Q	R	S	E	R	R	K	W	I	H	C	F	E	N	V	I	A	L	I	Y	L	A	S	L	S	E	Y	D	Q		G15
201	K	T	N	L	R	I	V	D	V	G	G	Q	K	S	E	R	K	K	W	I	H	C	F	E	N	V	I	A	L	I	Y	L	A	S	L	S	E	Y	D	Q		G16
238	V	L	V	E	S	D	N	E	N	R	M	E	E	S	K	A	L	F	R	T	I	I	T	Y	P	W	F	Q	N	S	S	V	I	L	F	L	N	K	K	D		hGq
241	C	L	E	E	N	D	Q	E	N	R	M	E	E	S	L	A	L	F	S	T	I	L	E	L	P	W	F	K	S	T	S	V	I	L	F	L	N	K	T	D		G15
241	C	L	E	E	N	N	Q	E	N	R	M	K	E	S	L	A	L	F	G	T	I	L	E	L	P	W	F	K	S	T	S	V	I	L	F	L	N	K	T	D		G16
278	L	L	E	E	K	I	M	Y	S	H	L	V	D	Y	F	P	E	Y	D	G	P	Q	R	D	A	Q	A	A	R	E	F	I	L	K	M	F	V	D	L	-	hGq	
281	I	L	E	D	K	I	H	T	S	H	L	A	T	Y	F	P	S	F	Q	G	P	R	R	D	A	E	A	A	K	S	F	I	L	D	M	Y	A	R	V	Y		G15
281	I	L	E	E	K	I	P	T	S	H	L	A	T	Y	F	P	S	F	Q	G	P	K	Q	D	A	E	A	A	K	R	F	I	L	D	M	Y	T	R	M	Y		G16
317	-	-	-	-	-	N	P	D	S	D	K	I	N	-	-	-	-	-	Y	S	H	F	T	C	A	T	D	T	E	N	I	R	F	V	F	A	A	V	K		hGq	
321	A	S	C	A	E	P	Q	D	G	G	R	K	G	S	R	A	R	R	F	F	A	H	F	T	C	A	T	D	T	Q	S	V	R	S	V	F	K	D	V	R		G15
321	T	G	C	V	D	G	P	E	G	S	K	K	G	A	R	S	R	R	L	F	S	H	Y	T	C	A	T	D	T	Q	N	I	R	K	V	F	K	D	V	R		G16
346	D	T	I	L	Q	L	N	L	K	E	Y	N	L	V																											hGq	
361	D	S	V	L	A	R	Y	L	D	E	I	N	L	L																											G15	
361	D	S	V	L	A	R	Y	L	D	E	I	N	L	L																											G16	

total = 4645660

Fig. 2. Amino acid sequences of the mouse and human $G\alpha_q$

1 = mouse
2 = human

1MTLESIMACCLSEEAKEARRINDEIER^QLRDKRDARRELKLLLGTGESGKSTFIKQMRIIHGS^GYSDE
2MTLESIMACCLSEEAKEARRINDEIER^QLRDKRDARRELKLLLGTGESGKSTFIKQMRIIHGS^GYSDE

DKRGFTKLVIYQNIPTAMQAMIRAMDTLKIPIKYEHNKAAQLVREVDVEKVSAF^{ENPYVD}AIKSLWNDPG
DKRGFTKLVIYQNIPTAMQAMIRAMDTLKIPIKYEHNKAAQLVREVDVEKVSAF^{ENPYVD}AIKSLWNDPG

IQECYDRRREYQLSDSTKYLLNDLDRVADPSYLPTQQDVLVRVPPTTGII EYPFDLQSVIFRMVDVGGQR
IQECYDRRREYQLSDSTKYLLNDLDRVADP^YYLPTQQDVLVRVPPTTGII EYPFDLQSVIFRMVDVGGQR

SERRKWIHCFENVTSIMFLValseyDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
SERRKWIHCFENVTSIMFLValseyDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE

EKIMYSHLVDYFPEYDGPQRDAQAAREFILKMFVDLNPDSKIIYSHFTCATDTENIRFVFAAVKDTILQ
EKIMYSHLVDYFPEYDGPQRDAQAAREFILKMFVDLNPDSKIIYSHFTCATDTENIRFVFAAVKDTILQ

LNLKEYNLV
LNLKEYNLV

Key amino acids described in this invention are boxed
Difference between human and mouse is underlined

Fig. 3. Amino acid sequences of the mouse and human $G\alpha_q$ proteins tested. Variation of amino acids of $G\alpha_q$ is depicted in parenthesis. The sequence numbers of amino acid H or Q, V or L are 28 and 29 respectively. The sequence number of amino acid G or D is 66. Truncation of N-terminal six amino acids (MTLESI) are shown as ΔN . Hemagglutinin (HA) epitope tag (DVPDYA) spans from 125 to 130. C-terminal five amino acids (-t5) or 44 amino acids (-t44) of transducin and five amino acids of $G\alpha_{olf}$ (-olf5) are used respectively to replace those of $G\alpha_q$.

Mouse sequences created and tested:

Sequence ID#1

mGq

MTLESI MACCLSEEAKEARRINDEIERQLRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSGYSDE
DKRGFTKL VYQNI FTAMQAMIRAMDTLKI PYKYEHNKAHAQLVREVDVEKVS AFENPYVDAIKSLWNDPG
IQECYDRRREYQLSDSTKYLLNDLDRVADPSYLP TQQDVL RVRVPTTGII EYPFDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLValseyDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDFPEYDGPQRDAQAAREFILKMFVDLNPDSDKIIYSHFTCATDTENIRFVFAAVKDTILQ
LNLKEYNLV

Sequence ID#2

mGq (ΔN)

MACCLSEEAKEARRINDEIERQLRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSGYSDE
DKRGFTKL VYQNI FTAMQAMIRAMDTLKI PYKYEHNKAHAQLVREVDVEKVS AFENPYVDAIKSLWNDPG
IQECYDRRREYQLSDSTKYLLNDLDRVADPSYLP TQQDVL RVRVPTTGII EYPFDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLValseyDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDFPEYDGPQRDAQAAREFILKMFVDLNPDSDKIIYSHFTCATDTENIRFVFAAVKDTILQ
LNLKEYNLV

Sequence ID#3

mGq (HA)

MTLESI MACCLSEEAKEARRINDEIERQLRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSGYSDE
DKRGFTKL VYQNI FTAMQAMIRAMDTLKI PYKYEHNKAHAQLVREVDVEKVS AFDPDYAAIKSLWNDPG
IQECYDRRREYQLSDSTKYLLNDLDRVADPSYLP TQQDVL RVRVPTTGII EYPFDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLValseyDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDFPEYDGPQRDAQAAREFILKMFVDLNPDSDKIIYSHFTCATDTENIRFVFAAVKDTILQ
LNLKEYNLV

Sequence ID#4

mGq (ΔN -HA)

MACCLSEEAKEARRINDEIERQLRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSGYSDE
DKRGFTKL VYQNI FTAMQAMIRAMDTLKI PYKYEHNKAHAQLVREVDVEKVS AFDPDYAAIKSLWNDPG
IQECYDRRREYQLSDSTKYLLNDLDRVADPSYLP TQQDVL RVRVPTTGII EYPFDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLValseyDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDFPEYDGPQRDAQAAREFILKMFVDLNPDSDKIIYSHFTCATDTENIRFVFAAVKDTILQ
LNLKEYNLV

Sequence ID#5

mGq (ΔN -HVD-HA) from Kostenis et al 1998

MACCLSEEAKEARRINDEIERHVRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSDYSDE
DKRGFTKL VYQNI FTAMQAMIRAMDTLKI PYKYEHNKAHAQLVREVDVEKVS AFDPDYAAIKSLWNDPG

IQECYDRRREYQLSDSTKYLLNDLDRVADPSYLPQQDVLVRVPPTGIIIEYFQDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLValseyDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDFPEYDGPQRDAQAAREFILKMFVDLNPDSKIIYSHFTCATDTENIRFVFAAVKDTILQ
LNLKEYNLV

Sequence ID#6

mGq (ΔN-HVD-HA) -t5

MACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSDYSDE
DKRGFTKLVIYQNI FTAMQAMIRAMDTLKIPIKYEHNAHAQLVREVDVEKVSADFVDPDYAAIKSLWNDPG
IQECYDRRREYQLSDSTKYLLNDLDRVADPSYLPQQDVLVRVPPTGIIIEYFQDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLValseyDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDFPEYDGPQRDAQAAREFILKMFVDLNPDSKIIYSHFTCATDTENIRFVFAAVKDTILQ
LNLKDCGLF

Sequence ID#7

mGq (ΔN-HVD-HA) -t44

MACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSDYSDE
DKRGFTKLVIYQNI FTAMQAMIRAMDTLKIPIKYEHNAHAQLVREVDVEKVSADFVDPDYAAIKSLWNDPG
IQECYDRRREYQLSDSTKYLLNDLDRVADPSYLPQQDVLVRVPPTGIIIEYFQDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLValseyDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDFPEYDGPQRDAQAAREFILKMFVDNMRDVEKIYSHMTCATDTQNVKFVDAVTDIIK
ENLKDCGLF

Sequence ID#8

mGq (ΔN-HVG-HA)

MACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSGYSDE
DKRGFTKLVIYQNI FTAMQAMIRAMDTLKIPIKYEHNAHAQLVREVDVEKVSADFVDPDYAAIKSLWNDPG
IQECYDRRREYQLSDSTKYLLNDLDRVADPSYLPQQDVLVRVPPTGIIIEYFQDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLValseyDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDFPEYDGPQRDAQAAREFILKMFVDLNPDSKIIYSHFTCATDTENIRFVFAAVKDTILQ
LNLKEYNLV

Sequence ID#9

mGq (HVG-HA)

MTLESIMACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSGYSDE
DKRGFTKLVIYQNI FTAMQAMIRAMDTLKIPIKYEHNAHAQLVREVDVEKVSADFVDPDYAAIKSLWNDPG
IQECYDRRREYQLSDSTKYLLNDLDRVADPSYLPQQDVLVRVPPTGIIIEYFQDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLValseyDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDFPEYDGPQRDAQAAREFILKMFVDLNPDSKIIYSHFTCATDTENIRFVFAAVKDTILQ
LNLKEYNLV

Sequence ID#10

mGq (D-HA)

MTLESIMACCLSEEAKEARRINDEIERQLRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSDYSDE
DKRGFTKLVIYQNI FTAMQAMIRAMDTLKIPIKYEHNAHAQLVREVDVEKVSADFVDPDYAAIKSLWNDPG
IQECYDRRREYQLSDSTKYLLNDLDRVADPSYLPQQDVLVRVPPTGIIIEYFQDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLValseyDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDFPEYDGPQRDAQAAREFILKMFVDLNPDSKIIYSHFTCATDTENIRFVFAAVKDTILQ
LNLKEYNLV

Sequence ID#11

mGq (HVD-HA)

MTLESIMACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSDYSDE
DKRGFTKL VYQNI FTAMQAMIRAMDTLKI PYKYEHNKAHAQLVREVDVEKVS AFDVDPDYAAIKSLWNDPG
IQECYDRRREYQLSDSTKY LNDLDRVADPSYLPTQQDVL RVRVPTTGIIEYPFDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLValseyDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDYFPEYDGPQRDAQAAREFILKMFVDLNPDSKIIYSHFTCATDTENIRFVFAAVKDTILQ
LNLKEYNLV

Sequence ID#12

mGq (HVG-HA) -t5

MTLESIMACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSGYSDE
DKRGFTKL VYQNI FTAMQAMIRAMDTLKI PYKYEHNKAHAQLVREVDVEKVS AFDVDPDYAAIKSLWNDPG
IQECYDRRREYQLSDSTKY LNDLDRVADPSYLPTQQDVL RVRVPTTGIIEYPFDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLValseyDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDYFPEYDGPQRDAQAAREFILKMFVDLNPDSKIIYSHFTCATDTENIRFVFAAVKDTILQ
LNLKDCGLF

Sequence ID#13

mGq (HVD-HA) -t5

MTLESIMACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSDYSDE
DKRGFTKL VYQNI FTAMQAMIRAMDTLKI PYKYEHNKAHAQLVREVDVEKVS AFDVDPDYAAIKSLWNDPG
IQECYDRRREYQLSDSTKY LNDLDRVADPSYLPTQQDVL RVRVPTTGIIEYPFDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLValseyDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDYFPEYDGPQRDAQAAREFILKMFVDLNPDSKIIYSHFTCATDTENIRFVFAAVKDTILQ
LNLKDCGLF

Sequence ID#14

mGq (ΔN-HVD-HA) -ol f5

MACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSDYSDE
DKRGFTKL VYQNI FTAMQAMIRAMDTLKI PYKYEHNKAHAQLVREVDVEKVS AFDVDPDYAAIKSLWNDPG
IQECYDRRREYQLSDSTKY LNDLDRVADPSYLPTQQDVL RVRVPTTGIIEYPFDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLValseyDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDYFPEYDGPQRDAQAAREFILKMFVDLNPDSKIIYSHFTCATDTENIRFVFAAVKDTILQ
LNLKQYELL

Human Sequences Tested

Sequence ID#15

hGq

MTLESIMACCLSEEAKEARRINDEIERQLRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSGYSDE
DKRGFTKL VYQNI FTAMQAMIRAMDTLKI PYKYEHNKAHAQLVREVDVEKVS AFENPYVDAIKSLWNDPG
IQECYDRRREYQLSDSTKY LNDLDRVADPAYLPTQQDVL RVRVPTTGIIEYPFDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLValseyDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDYFPEYDGPQRDAQAAREFILKMFVDLNPDSKIIYSHFTCATDTENIRFVFAAVKDTILQ
LNLKEYNAV

Sequence ID#16

hGq (ΔN)

MACCLSEEAKEARRINDEIERQLRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSGYSDE
DKRGFTKL VYQNI FTAMQAMIRAMDTLKI PYKYEHNKAHAQLVREVDVEKVS AFENPYVDAIKSLWNDPG
IQECYDRRREYQLSDSTKY LNDLDRVADPAYLPTQQDVL RVRVPTTGIIEYPFDLQSVIFRMVDVGGQR

SERRKWIHC FENVTSIMFLValseyDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
 EKIMYSHLVDFPEYDGPQRDAQAAREFILKMFVDLNPDSDKIIYSHFTCATDTENIRFVFAAVKDTILO
 LNLKEYNAV

Table I: Function Activity Of Gq Variants Tested

Gq Variants	Seq ID #	Functional Activity with Taste Receptor mT2R5	Functional Activity with Olfactory Receptor mI7
mGq	1	-	Not tested
mGq(Δ N)	2	-	Not tested
mGq(HA)	3	-	Not tested
mGq(Δ N-HA)	4	-	Not tested
mGq(Δ N-HVD-HA)	5	+	+
mGq(Δ N-HVD-HA)-t5	6	++	Not tested
mGq(Δ N-HVD-HA)-t44	7	++	Not tested
mGq(Δ N-HV-HA)	8	-	Not tested
mGq(HV-HA)	9	-	Not tested
mGq(D-HA)	10	+	Not tested
mGq(HVD-HA)	11	+	Not tested
mGq(HV-HA)-t5	12	+	Not tested
mGq(HVD-HA)-t5	13	++	Not tested
mGq(Δ N-HVD-HA)-olf5	14	Not tested	++
hGq	15	-	Not tested
hGq(Δ N)	16	-	Not tested

+ means functionally couples with chemosensory receptor
 ++ means functionally couples with chemosensory receptor
 - means does not functionally couple

Figure 4. Other sequences predicted by this invention active in assays of chemosensory receptors such as those GPCRs involved in sensing of tastants, olfactants and pheromones.

Sequence ID#17

hGq (Δ N-HVD-HA)

MACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSDYSDE
DKRGFTKLVIYQNIIFTAMQAMIRAMDTLKIPIKYEHNKAAHAQLVREVDVEKVSADFVDPDYAAIKSLWNDPG
IQECYDRRREYQLSDSTKYLLNDLDRVADPAYLPTQQDVLVRVPPTGIIIEYPFDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLValseyDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDYFPEYDGPQRDAQAAREFILKMFVDLNPDSKIIYSHFTCATDTENIRFVFAAVKDTILQ
LNLKEYNLV

Sequence ID#18

hGq (Δ N-HVD-HA) -t5

MACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSDYSDE
DKRGFTKLVIYQNIIFTAMQAMIRAMDTLKIPIKYEHNKAAHAQLVREVDVEKVSADFVDPDYAAIKSLWNDPG
IQECYDRRREYQLSDSTKYLLNDLDRVADPAYLPTQQDVLVRVPPTGIIIEYPFDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLValseyDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDYFPEYDGPQRDAQAAREFILKMFVDLNPDSKIIYSHFTCATDTENIRFVFAAVKDTILQ
LNLKDCGLF

Sequence ID#19

hGq (Δ N-HVD-HA) -t44

MACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSDYSDE
DKRGFTKLVIYQNIIFTAMQAMIRAMDTLKIPIKYEHNKAAHAQLVREVDVEKVSADFVDPDYAAIKSLWNDPG
IQECYDRRREYQLSDSTKYLLNDLDRVADPAYLPTQQDVLVRVPPTGIIIEYPFDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLValseyDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDYFPEYDGPQRDAQAAREFILKMFVDNMRDVKEIYSHMTCATDTQNVKFVFDVAVTDIIK
ENLKDCGLF

Sequence ID#20

hGq (D-HA)

MTLESIMACCLSEEAKEARRINDEIERQLRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSDYSDE
DKRGFTKLVIYQNIIFTAMQAMIRAMDTLKIPIKYEHNKAAHAQLVREVDVEKVSADFVDPDYAAIKSLWNDPG
IQECYDRRREYQLSDSTKYLLNDLDRVADPAYLPTQQDVLVRVPPTGIIIEYPFDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLValseyDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDYFPEYDGPQRDAQAAREFILKMFVDLNPDSKIIYSHFTCATDTENIRFVFAAVKDTILQ
LNLKEYNLV

Sequence ID#21

hGq (HVD-HA)

MTLESIMACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSDYSDE
DKRGFTKLVIYQNIIFTAMQAMIRAMDTLKIPIKYEHNKAAHAQLVREVDVEKVSADFVDPDYAAIKSLWNDPG
IQECYDRRREYQLSDSTKYLLNDLDRVADPAYLPTQQDVLVRVPPTGIIIEYPFDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLValseyDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDYFPEYDGPQRDAQAAREFILKMFVDLNPDSKIIYSHFTCATDTENIRFVFAAVKDTILQ
LNLKEYNLV

Sequence ID#22

hGq (HVG-HA) -t5

MTLESIMACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSGYSDE
DKRGFTKLVIYQNI FTAMQAMIRAMDTLKI PYKYEHNKAAHQLVREVDVEKVS AFDVDPDYAAIKSLWNDPG
IQECYDRRREYQLSDSTKYLLNDLDRVADPAYLPTQQDVLVRVPPTGII EYPFDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLValseyDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDFPEYDGPQRDAQAAREFILKMFVDLNPDSDKIIYSHFTCATDTENIRFVFAAVKDTILO
LNLKDCGLF

Sequence ID#23

hGq (HVD-HA) -t5

MTLESIMACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSDYSDE
DKRGFTKLVIYQNI FTAMQAMIRAMDTLKI PYKYEHNKAAHQLVREVDVEKVS AFDVDPDYAAIKSLWNDPG
IQECYDRRREYQLSDSTKYLLNDLDRVADPAYLPTQQDVLVRVPPTGII EYPFDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLValseyDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDFPEYDGPQRDAQAAREFILKMFVDLNPDSDKIIYSHFTCATDTENIRFVFAAVKDTILO
LNLKDCGLF

Sequence ID#24

hGq (ΔN-HVD-HA) -ol f5

MACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSDYSDE
DKRGFTKLVIYQNI FTAMQAMIRAMDTLKI PYKYEHNKAAHQLVREVDVEKVS AFDVDPDYAAIKSLWNDPG
IQECYDRRREYQLSDSTKYLLNDLDRVADPAYLPTQQDVLVRVPPTGII EYPFDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLValseyDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDFPEYDGPQRDAQAAREFILKMFVDLNPDSDKIIYSHFTCATDTENIRFVFAAVKDTILO
LNLKQYELL

Sequence ID#25

hGq (HVG-HA) -t5

MTLESIMACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSGYSDE
DKRGFTKLVIYQNI FTAMQAMIRAMDTLKI PYKYEHNKAAHQLVREVDVEKVS AFDVDPDYAAIKSLWNDPG
IQECYDRRREYQLSDSTKYLLNDLDRVADPAYLPTQQDVLVRVPPTGII EYPFDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLValseyDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDFPEYDGPQRDAQAAREFILKMFVDLNPDSDKIIYSHFTCATDTENIRFVFAAVKDTILO
LNLKQYELL

Sequence ID#26

hGq (HVD-HA) -t5

MTLESIMACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSDYSDE
DKRGFTKLVIYQNI FTAMQAMIRAMDTLKI PYKYEHNKAAHQLVREVDVEKVS AFDVDPDYAAIKSLWNDPG
IQECYDRRREYQLSDSTKYLLNDLDRVADPAYLPTQQDVLVRVPPTGII EYPFDLQSVIFRMVDVGGQR
SERRKWIHCFENVTSIMFLValseyDQVLVESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLE
EKIMYSHLVDFPEYDGPQRDAQAAREFILKMFVDLNPDSDKIIYSHFTCATDTENIRFVFAAVKDTILO
LNLKQYELL